*182078*  *MS*

# STIC-Biotech/ChemLib

**From:** Chernyshev, Olga
**Sent:** Monday, March 13, 2006 4:47 PM
**To:** STIC-Biotech/ChemLib
**Subject:** 10/721,297, sequence search request

**Please search SEQ ID NO: 1 and SEQ ID NO: 10 in regular databases only.
Thank you very much!**

*Olga N. Chernyshev, Ph.D.*
*AU 1649*
*REM 3C89*
*2-0870*
*mail 4C70*

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```
OM protein - protein search, using sw model

                    Copyright (c) 1993 - 2006 Bioacceleration Ltd.;
                    GenCore version 5.1.7

Run on:             March 15, 2006, 20:08:12 ; Search time 146.5 Seconds
                    (without alignments)
                    33.711 Million cell updates/sec

Title:              US-10-721-297-1
Perfect score:      34
Sequence:           1 EVKMDAE 7

Scoring table:      BLOSUM62
                    Gapop 10.0 , Gapext 0.5

Searched:           2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters:   2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :          UniProt_05.80:*
                    1: uniprot_sprot:*
                    2: uniprot_trembl:*

                              SUMMARIES

                    Query
Result    Score     Match Length DB  ID          Description
No.
------    -----     ------------ --  --          -----------
  1        34       57      1     Q29149 u alzheimer
  2        34       58      1     A4_CANFA
  3        34       58      1     A4_RABIT     Q28280 o alzheimer
  4        34       58      1     A4_SHEEP     Q28748 o alzheimer
  5        34       59      1     A4_BOVIN     Q28757 o alzheimer
  6        34       79      1     O35463_CRIGR  Q28053 b alzheimer
  7        34      113      1     O8JH58_CHESE  O35463 cricetulus
  8        34      218      2     O8JH58_CHESE chelydra se
  9        34      384      2     O8BPC7_MOUSE  O8jh58 chelydra se
 10        34      534      2     O93296_CHICK  O8bpc7 mus musculu
 11        34      569      2     O9PVL1_CHICK  O93296 gallus gall
 12        34      695      2     O5R477_PONPY  O9pvl1 gallus gall
 13        34      695      2     A4_SAISC     O5r477 pongo pygma
 14        34      695      2     O6GR78_MOUSE  A4_SAISC saimiri
 15        34      695      2     O9DGJ8_CHICK  O6gr78 mus musculu
 16        34      695      2     O9DGJ8_CHICK  O9dgj8 gallus gall
 17        34      714      2     O56JK4_CANFA  O9dgj8 gallus gall
 18        34      733      2     O56JK2_STECO  O6p6q5 rattus norv
 19        34      749      1     A4_SAISC     O95241 s amyloid b
 20        34      751      1     O6SCO_HUMAN  O6gsco homo sapien
 21        34      751      2     O6RH28_CANFA  O6rh28 canis famil
 22        34      751      2     O56JK5_CANFA  O56jk5 canis famil
 23        34      751      2     Q4R4R8_MACFA  O4r4r8 macaca fasc
 24        34      751      2     O9DGJ7_CHICK  O9dgj7 gallus gall
 25        34      751      2     O60495_C     O60495 c amyloid b
 26        34      770      1     A4_CAVPO     P05067 h amyloid b
 27        34      770      1     A4_HUMAN     P05067 h amyloid b
 28        34      770      1     A4_MACFA     P53601 m amyloid b
 29        34      770      1     A4_MACFA     P12023 m amyloid b
 30        34      770      1     A4_PANTR     Q5is80 p amyloid b
 31        34      770      1     A4_PIG       P79307 s amyloid b
 32        34      770      1     P08592 r amyloid b
 33        34      770      2     Q6RH30_CANFA  Q6rh30 canis famil
 34        34      770      2     Q56JK6_CANFA  Q56jk6 canis famil
 35        34      770      2     Q532T3_MOUSE  Q532t3 mus musculu
 36        34      770      2     Q547B7_RAT    Q547b7 rattus norv
 37        34      119      2     Q82ZP0_PYRAE  Q82zp0 pyrobaculum
 38        31      336      2     Q6PC00_BRARE  Q6pc00 brachydanio
 39        31      354      2     Q4SK78_TETNG  Q4sk78 tetraodon n
 40        31      693      2     Q98SG0_XENLA  Q98sg0 xenopus lae
 41        31      695      2     Q98SF9_XENLA  Q98sf9 xenopus lae
 42        31      695      2     Q7ZXQ0_XENLA  Q7zxq0 xenopus lae
 43        31      747      2     Q91963_XENLA  Q91963 xenopus. ap
 44        31      749      2     Q6NRR1_XENLA  Q6nrr1 xenopus lae
 45        31      750      2     Q6DJB6_XENTR  Q6djb6 xenopus tro
```

ALIGNMENTS

```
RESULT 1
ID    A4_URSMA                   STANDARD;      PRT;    57 AA.
AC    Q29149;
DT    01-NOV-1997 (Rel. 35, Created)
DT    01-NOV-1997 (Rel. 35, Last sequence update)
DT    10-MAY-2005 (Rel. 47, Last annotation update)
DE    Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE    beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE    Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(57) (Gamma-secretase
DE    C-terminal fragment 59) (fragment).
DE    fragment 57)] (fragment).
GN    Name=APP;
OS    Ursus maritimus (Polar bear) (Thalarctos maritimus).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Ursidae;
OC    Ursus.
OX    NCBI_TaxID=29073;
RN    [1]
RP    NUCLEOTIDE SEQUENCE.
RC    TISSUE=Brain;
RX    MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA    Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT    "Conservation of the sequence of the Alzheimer's disease amyloid
RT    peptide in dog, polar bear and five other mammals by cross-species
RT    polymerase chain reaction analysis.";
RL    Brain Res. Mol. Brain Res. 10:299-305(1991).
CC    -!- FUNCTION: Functional neuronal receptor which couples to
CC        intracellular signaling pathway through the GTP-binding protein
CC        G(O) (By similarity).
CC    -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC    -!- SIMILARITY: Belongs to the APP family.
CC    --------------------------------------------------------------------------
CC    This Swiss-Prot entry is copyright. It is produced through a collaboration
CC    between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC    the European Bioinformatics Institute.  There are no restrictions on its
CC    use as long as its content is in no way modified and this statement is not
CC    removed.
CC    --------------------------------------------------------------------------
DR    EMBL; X56128; CAA39593.1; -; mRNA.
DR    PIR; B60045; B60045.
DR    HSSP; P08592; 1NMJ.
DR    InterPro; IPR000155; A4_APP.
DR    InterPro; IPR001255; Beta-APP.
DR    PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR    Pfam; PF03494; Beta-APP; 1.
DR    PRINTS; PR00204; BETAAMYLOID.
DR    PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR    PROSITE; PS00320; A4_INTRA; PARTIAL.
KW    Amyloid; Transmembrane.
FT    CHAIN         1      5       Soluble APP-beta (By similarity).
FT    CHAIN        <1      5       CTF-alpha (By similarity).
FT    CHAIN         6     >57      Beta-amyloid protein 42 (By similarity).
FT    CHAIN         6      47      Beta-amyloid protein 40 (By similarity).
FT    CHAIN         6      45      Beta-amyloid protein 40 (By similarity).
```

## RESULT 2

```
Qy    1 EVRKMDAE 7
        |||||||
Db    2 EVRKMDAE 8
```

Query Match          100.0%;
Best Local Similarity 100.0%;
Matches   7; Conservative   0;

Score 34; DB 1; Length 57;
Best Local Similarity 100.0%;
Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
SQ   SEQUENCE   57 AA;  6172 MW;  84209D88EBA82DFA CRC64;
FT   NON_TER       1
FT   NON_TER      57
FT   TRANSMEM     34     57       Potential.
FT   TOPO_DOM      1     33       Extracellular (Potential).
FT   CHAIN        48    >57       Gamma-CTF(59) (By similarity).
FT   CHAIN        46    >57       Gamma-CTF(57) (By similarity).
```

```
ID   A4_CANFA     STANDARD;      PRT;    58 AA.
AC   Q28280;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE   beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE   Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE   C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE   fragment 57)] (Fragment).
GN   Name=APP;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC   Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RX   MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: Functional neuronal receptor which couples to
CC       intracellular signaling pathway through the GTP-binding protein
CC       G(O) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   -----------------------------------------------------------------------
DR   EMBL; X56125; CAA39590.1; -; mRNA.
DR   HSSP; P08592; 1NMJ.
DR   Ensembl; ENSCAFG00000008557; Canis familiaris.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00204; BETAAMYLOID.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
KW   Amyloid; Transmembrane.
FT   CHAIN        <1      6       Soluble APP-beta (By similarity).
FT   CHAIN         7    >58       CTF-alpha (By similarity).
FT   CHAIN         7     48       Beta-amyloid protein 42 (By similarity).
FT   CHAIN         7     46       Beta-amyloid protein 40 (By similarity).
FT   CHAIN        47    >58       Gamma-CTF(59) (By similarity).
FT   CHAIN        49    >58       Gamma-CTF(57) (By similarity).
```

## RESULT 3

```
Qy    1 EVRKMDAE 7
        |||||||
Db    3 EVRKMDAE 9
```

Query Match          100.0%;
Best Local Similarity 100.0%;
Matches   7; Conservative   0;

Score 34; DB 1; Length 58;
Best Local Similarity 100.0%;
Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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SQ   SEQUENCE   58 AA;  6285 MW;  84690488A2E12DFA CRC64;
FT   TOPO_DOM     <1     34       Extracellular (Potential).
FT   TRANSMEM     35     58       Potential.
FT   NON_TER       1
FT   NON_TER      58
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ID   A4_RABIT     STANDARD;      PRT;    58 AA.
AC   Q28748;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE   beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE   Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE   C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE   fragment 57)] (Fragment).
GN   Name=APP;
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC   Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RX   MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: Functional neuronal receptor which couples to
CC       intracellular signaling pathway through the GTP-binding protein
CC       G(O) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   -----------------------------------------------------------------------
DR   EMBL; X56129; CAA39594.1; -; mRNA.
DR   HSSP; P08592; 1NMJ.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00204; BETAAMYLOID.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
KW   Amyloid; Transmembrane.
FT   CHAIN        <1      5       Soluble APP-beta (By similarity).
FT   CHAIN         6    >58       CTF-alpha (By similarity).
FT   CHAIN         6     47       Beta-amyloid protein 42 (By similarity).
FT   CHAIN         6     45       Beta-amyloid protein 40 (By similarity).
FT   CHAIN        46    >58       Gamma-CTF(59) (By similarity).
FT   CHAIN        48    >58       Gamma-CTF(57) (By similarity).
FT   TOPO_DOM     <1     33       Extracellular (Potential).
FT   TRANSMEM     34     57       Potential.
FT   TOPO_DOM     58             Cytoplasmic (Potential).
```

GenCore version 5.1.7

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OM protein - protein search, using sw model

Run on:          March 15, 2006, 20:07:46 ; Search time 135 Seconds
                 (without alignments)
                 22.783 Million cell updates/sec

Title:           US-10-721-297-1
Perfect Score:   34
Sequence:        1 EVRMDAE 7

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters:          2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       A_Geneseq_21:*
                 1: geneseqp1980s:*
                 2: geneseqp1990s:*
                 3: geneseqp2000s:*
                 4: geneseqp2001s:*
                 5: geneseqp2002s:*
                 6: geneseqp2003as:*
                 7: geneseqp2003bs:*
                 8: geneseqp2004s:*
                 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 34 | 100.0 | 7 | 8 | ADJ71532 | Adj71532 N-termina |
| 2 | 34 | 100.0 | 7 | 9 | AEA23387 | Aea23387 Human APP |
| 3 | 34 | 100.0 | 8 | 3 | AAY94772 | Aay94772 Beta-secr |
| 4 | 34 | 100.0 | 8 | 9 | AAU07230 | Aau07230 Human APP |
| 5 | 34 | 100.0 | 8 | 4 | AAB10660 | Aab10660 Human Asp |
| 6 | 34 | 100.0 | 8 | 4 | AAE06902 | Aae06902 Human amy |
| 7 | 34 | 100.0 | 8 | 4 | AAE02612 | Aae02612 Human Asp |
| 8 | 34 | 100.0 | 8 | 4 | AAU06635 | Aau06635 Synthetic |
| 9 | 34 | 100.0 | 8 | 4 | AAU06631 | Aau06631 Beta secr |
| 10 | 34 | 100.0 | 8 | 5 | ABB78621 | Abb78621 APP Swedi |
| 11 | 34 | 100.0 | 8 | 8 | ADJ71533 | Adj71533 N-termina |
| 12 | 34 | 100.0 | 8 | 8 | ADJ71545 | Adj71545 N-termina |
| 13 | 34 | 100.0 | 8 | 8 | ADJ94379 | Adj94379 Human amy |
| 14 | 34 | 100.0 | 8 | 8 | ADO50475 | Ado50475 Substrate |
| 15 | 34 | 100.0 | 8 | 8 | ADR75388 | Adr75388 Substrate |
| 16 | 34 | 100.0 | 8 | 9 | ADU82824 | Adu82824 Human APP |
| 17 | 34 | 100.0 | 8 | 9 | AEA23384 | Aea23384 Human APP |
| 18 | 34 | 100.0 | 9 | 2 | AAW82083 | Aaw82083 Fluorogen |
| 19 | 34 | 100.0 | 9 | 3 | AAY87949 | Aay87949 Mammalian |
| 20 | 34 | 100.0 | 9 | 3 | AAB07873 | Aab07873 A peptide |
| 21 | 34 | 100.0 | 9 | 5 | ABU60430 | Abu60430 Protease |
| 22 | 34 | 100.0 | 9 | 7 | ADC26556 | Adc26556 Beta-secr |
| 23 | 34 | 100.0 | 9 | 8 | ADJ71534 | Adj71534 N-termina |
| 24 | 34 | 100.0 | 9 | 8 | ADJ71557 | Adj71557 N-termina |
| 25 | 34 | 100.0 | 9 | 8 | ADJ71546 | Adj71546 N-termina |
| 26 | 34 | 100.0 | 9 | 8 | ADS18111 | Ads18111 Amyloid p |
| 27 | 34 | 100.0 | 9 | 9 | AEA35404 | Aea35404 QC inhibi |
| 28 | 34 | 100.0 | 9 | 8 | AAR22054 | Aar22054 Peptide P |
| 29 | 34 | 100.0 | 10 | 2 | AAR24261 | Aar24261 Human amy |
| 30 | 34 | 100.0 | 10 | 2 | AAW82440 | Aaw82440 Human amy |
| 31 | 34 | 100.0 | 10 | 3 | AAY69703 | Aay69703 Beta-APP |
| 32 | 34 | 100.0 | 10 | 4 | AAU07227 | Aau07227 Human bet |
| 33 | 34 | 100.0 | 10 | 4 | AAE10654 | Aae10654 Human wil |
| 34 | 34 | 100.0 | 10 | 4 | AAE06899 | Aae06899 Human amy |
| 35 | 34 | 100.0 | 10 | 4 | AAB46208 | Aab46208 Human APP |
| 36 | 34 | 100.0 | 10 | 4 | AAB46207 | Aab46207 Human APP |
| 37 | 34 | 100.0 | 10 | 4 | AAB46209 | Aab46209 Human APP |
| 38 | 34 | 100.0 | 10 | 4 | AAB46206 | Aab46206 Human APP |
| 39 | 34 | 100.0 | 10 | 4 | AAB61336 | Aab61336 Sythetic |
| 40 | 34 | 100.0 | 10 | 2 | AAE02606 | Aae02606 Human wil |
| 41 | 34 | 100.0 | 10 | 4 | AAB66574 | Aab66574 Synthetic |
| 42 | 34 | 100.0 | 10 | 4 | AAG62668 | Aag62668 Beta-shee |
| 43 | 34 | 100.0 | 10 | 4 | AAU06628 | Aau06628 Asp2 reco |
| 44 | 34 | 100.0 | 10 | 5 | ABB06426 | Abb06426 Human APP |
| 45 | 34 | 100.0 | 10 | 5 | ABG78375 | Abg78375 Human bet |

ALIGNMENTS

RESULT 1
ADJ71532

ID    ADJ71532 standard; peptide; 7 AA.

XX

AC    ADJ71532;

XX

DT    06-MAY-2004  (first entry)

XX

DE    N-terminal APP peptide C-terminal fragment, SEQ ID 195.

XX

KW    Nootropic; Neuroprotective; Vaccine; beta Amyloid;
KW    amyloid precursor protein; APP; Alzheimer's disease.

XX

OS    Homo sapiens.

XX

PN    WO2004013172-A2.

XX

PD    12-FEB-2004.

XX

PF    18-JUL-2003; 2003WO-EP007833.

XX

PR    24-JUL-2002; 2002EP-00447147.
PR    06-AUG-2002; 2002US-0401497P.

XX

PA    (INNO-) INNOGENETICS NV.

XX

PI    Delacourte A, Sergeant N;

XX

DR    WPI; 2004-180423/17.

XX

PT    New beta-amyloid or amyloid precursor protein preparation, useful as a
PT    prophylactic vaccine or a therapeutic for preventing or treating a
PT    disease associated with beta-amyloid formation and/or aggregation, e.g.
PT    Alzheimer's disease.

XX

PS    Claim 7; Page 66; 104pp; English.

XX

CC    The present invention relates to preparations (I) comprising a beta-
CC    amyloid peptide variant or beta-amyloid N-terminal fragment, or N-
CC    terminal amyloid precursor protein (APP) soluble fragment or C-terminal
CC    fragment. The beta-amyloid or APP preparations are useful for
CC    manufacturing a prophylactic vaccine or a therapeutic, or as a
CC    prophylactic vaccine for the prevention, or as a therapeutic for the
CC    treatment of a disease associated with beta-amyloid formation and/or
CC    aggregation, such as Alzheimer's disease.

XX

SQ    Sequence 7 AA;

Qy    1 EVKMDAE 7
        |||||||
Db    1 EVKMDAE 7

RESULT 2
```
Query Match          100.0%; Score 34; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches    7; Conservative  0; Mismatches  0; Indels  0; Gaps  0;
```

ID   AEA23387 standard; peptide; 7 AA.
XX
AC   AEA23387;
XX
DT   28-JUL-2005 (first entry)
XX
DE   Human APP beta-secretase cleavage site peptide #2.
XX
KW   Screening; beta-amyloid; amyloid precursor protein; neuroprotective;
KW   nootropic; degeneration; neurological disease; beta-secretase.
XX
OS   Homo sapiens.
XX
PN   US2005112696-A1.
XX
PD   26-MAY-2005.
XX
PF   25-NOV-2003; 2003US-00721297.
PR   25-NOV-2003; 2003US-00721297.
XX
PA   (UYTE-) UNIV TEXAS SOUTHWESTERN MEDICAL CENT DAL.
XX
PI   Sudhof TC, Li Q;
XX
DR   WPI; 2005-403362/41.
XX
PT   Identifying agents modulating cleavage of amyloid beta-precursor protein
PT   by beta-secretase, by contacting chimeric molecule comprising cleavage
PT   site with beta-secretase in presence of modulating agent, measuring
PT   nuclear localization.
XX
PS   Claim 2; Page 10; 20pp; English.
XX
CC   The present invention relates to a method of screening and identifying
CC   agents that modulate cleavage of amyloid beta-precursor protein (APP) or
CC   APP-like proteins such as APLP1 and APLP2 by a beta-secretase. The method
CC   involves contacting a chimeric molecule comprising a transmembrane region
CC   (TMR) with a gamma- or beta-secretase cleavage site and an APP C-
CC   terminal cytoplasmic tail modified with beta-secretase in presence and
CC   absence of a modulating agent and identifying cleavage by measuring
CC   nuclear localization of C-terminal cytoplasmic tail. The invention is
CC   useful in the treatment of Alzheimer's disease. The present sequence is
CC   the human APP beta-secretase cleavage site peptide.
XX
SQ   Sequence 7 AA;

RESULT 3

Qy    1 EVKMDAE 7
        |||||||
Db    1 EVKMDAE 7

```
Query Match          100.0%; Score 34; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches    7; Conservative  0; Mismatches  0; Indels  0; Gaps  0;
```

ID   AAY94772 standard; protein; 8 AA.
XX
AC   AAY94772;

DT   12-FEB-2001 (first entry)
XX
DE   Beta-secretase substrate peptide SEQ ID 18.
XX
KW   Beta-secretase; enzyme; amyloid plaque; Alzheimer's disease;
KW   Down's syndrome; amyloid angiopathy; gene therapy; neuroprotective.
XX
OS   Synthetic.
XX
PN   WO200058479-A1.
XX
PD   05-OCT-2000.
XX
PF   23-MAR-2000; 2000WO-US007755.
XX
PR   26-MAR-1999;  99US-00277229.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Citron M, Vassar RJ, Bennett BD;
XX
DR   WPI; 2000-594643/56.
XX
PT   Isolated beta-secretase nucleic acids and encoded polypeptides, useful
PT   for diagnosis and gene therapy of Alzheimer's disease.
XX
PS   Example 10; Page 117; 145pp; English.
XX
CC   This invention relates to 3 nucleotide sequences encoding beta-secretase
CC   proteins. Beta-secretase is an enzyme involved in the production of one
CC   of the components of amyloid plaques involved in Alzheimer's disease. The
CC   invention includes an expression vector comprising the nucleotide
CC   sequence, a host cell comprising the expression vector, and a process for
CC   producing the protein through culturing the transformed cells. Also
CC   included in the invention are a polypeptide derivative of the beta-
CC   secretase protein, a fusion protein comprising beta-secretase fused to a
CC   heterologous amino acid sequence, and a method for modulating the levels
CC   of beta-secretase polypeptide in a mammal comprising administering the
CC   polynucleotide sequence. Beta-secretase exhibits neuroprotective and
CC   nootropic activity. The beta-secretase nucleotide sequence may be used to
CC   map locations of the beta-secretase gene and related genes on chromosomes
CC   and as hybridization probes in diagnostic assays to test for the presence
CC   of beta-secretase DNA or RNA, such as in Alzheimer's disease, Down's
CC   syndrome, and amyloid angiopathy. The nucleotide sequence may also be
CC   used as anti-sense inhibitors of beta-secretase expression, in gene
CC   therapy of Alzheimer's disease, and for the identification of compounds
CC   that modulate beta-secretase activity. Antibodies to the beta-secretase
CC   protein may be used for in vitro and in vivo diagnostic purposes to
CC   detect the presence of beta-secretase polypeptide in a body fluid or cell
CC   sample. The present sequence represents a beta-secretase substrate
CC   peptide.
XX
SQ   Sequence 8 AA;

RESULT 4

Qy    1 EVKMDAE 7
        |||||||
Db    1 EVKMDAE 7

```
Query Match          100.0%; Score 34; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches    7; Conservative  0; Mismatches  0; Indels  0; Gaps  0;
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ID   AAU07230 standard; peptide; 8 AA.
XX
AC   AAU07230;
XX
DT   24-OCT-2001 (first entry)
XX
DE   Human beta-amyloid protein precursor, APP-beta secretase site peptide #3.

# Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.

- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

  http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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RESULT 3
US-09-551-853D-67
; Sequence 67, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Peptide
US-09-551-853D-67

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Best Local Similarity   100.0%;  Pred. No. 4.6e+05;
Matches    7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy          1 EVKMDAE 7
              |||||||
Db          1 EVKMDAE 7

RESULT 4
US-09-416-901B-67
; Sequence 67, Application US/09416901B
; Patent No. 6699671
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280A

RESULT 5
US-09-548-376D-67
; Sequence 67, Application US/09548376D
; Patent No. 6706485
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
; TITLE OF INVENTION: AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280F
; CURRENT APPLICATION NUMBER: US/09/548,376D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthesized peptide
US-09-548-376D-67

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Best Local Similarity   100.0%;  Pred. No. 4.6e+05;
Matches    7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy          1 EVKMDAE 7
              |||||||
Db          1 EVKMDAE 7

RESULT 6
US-09-794-927A-67
; Sequence 67, Application US/09794927A
; Patent No. 6727074
; GENERAL INFORMATION:

PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Peptide
US-09-548-367D-67

Query Match             100.0%;  Score 34;  DB 2;  Length 8;
Best Local Similarity   100.0%;  Pred. No. 4.6e+05;
Matches    7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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              |||||||
Db          1 EVKMDAE 7

; CURRENT APPLICATION NUMBER: US/09/416,901B
; CURRENT FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-416-901B-67

Query Match             100.0%;  Score 34;  DB 2;  Length 8;
Best Local Similarity   100.0%;  Pred. No. 4.6e+05;
Matches    7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy          1 EVKMDAE 7
              |||||||
Db          1 EVKMDAE 7

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on:          March 15, 2006, 20:17:57 ; Search time 33.5 Seconds
                                            (without alignments)
                                            17.276 Million cell updates/sec

Title:           US-10-721-297-1
Perfect score:   34
Sequence:        1 EVKMDAE 7
Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5
Searched:        572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters:     572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Issued Patents AA:*
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                 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
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                 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 5: /cgn2_6/ptodata/1/iaa/RB_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
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| 2 | 34 | 100.0 | 8 | 2 | US-09-548-367D-67 | Sequence 67, Appli |
| 3 | 34 | 100.0 | 8 | 2 | US-09-551-853D-67 | Sequence 67, Appli |
| 4 | 34 | 100.0 | 8 | 2 | US-09-416-901B-67 | Sequence 67, Appli |
| 5 | 34 | 100.0 | 8 | 2 | US-09-548-376D-67 | Sequence 67, Appli |
| 6 | 34 | 100.0 | 8 | 2 | US-09-794-927A-67 | Sequence 67, Appli |
| 7 | 34 | 100.0 | 8 | 2 | US-09-548-373D-67 | Sequence 67, Appli |
| 8 | 34 | 100.0 | 8 | 2 | US-09-795-847B-67 | Sequence 67, Appli |
| 9 | 34 | 100.0 | 8 | 2 | US-09-869-414-67 | Sequence 67, Appli |
| 10 | 34 | 100.0 | 8 | 2 | US-09-548-366F-67 | Sequence 67, Appli |
| 11 | 34 | 100.0 | 8 | 2 | US-09-548-368D-67 | Sequence 67, Appli |
| 12 | 34 | 100.0 | 8 | 2 | US-09-794-925A-67 | Sequence 67, Appli |
| 13 | 34 | 100.0 | 8 | 2 | US-09-668-314C-70 | Sequence 70, Appli |
| 14 | 34 | 100.0 | 8 | 2 | US-09-794-743-67 | Sequence 67, Appli |
| 15 | 34 | 100.0 | 9 | 2 | US-08-802-981-221 | Sequence 221, App |
| 16 | 34 | 100.0 | 9 | 2 | US-09-294-987-6 | Sequence 6, Appli |
| 17 | 34 | 100.0 | 9 | 2 | US-09-724-566A-82 | Sequence 82, Appli |
| 18 | 34 | 100.0 | 9 | 2 | US-09-471-669A-82 | Sequence 82, Appli |
| 19 | 34 | 100.0 | 10 | 1 | US-08-025-321C-1 | Sequence 1, Appli |
| 20 | 34 | 100.0 | 10 | 2 | US-09-548-372D-64 | Sequence 64, Appli |
| 21 | 34 | 100.0 | 10 | 2 | US-09-551-853D-64 | Sequence 64, Appli |
| 22 | 34 | 100.0 | 10 | 2 | US-09-548-367D-64 | Sequence 64, Appli |
| 23 | 34 | 100.0 | 10 | 2 | US-09-416-901B-64 | Sequence 64, Appli |
| 24 | 34 | 100.0 | 10 | 2 | US-09-604-608-4 | Sequence 4, Appli |
| 25 | 34 | 100.0 | 10 | 2 | US-09-548-376D-64 | Sequence 64, Appli |
| 26 | 34 | 100.0 | 10 | 2 | US-09-794-927A-64 | Sequence 64, Appli |
| 27 | 34 | 100.0 | 10 | 2 | US-09-548-373D-64 | Sequence 64, Appli |
| 28 | 34 | 100.0 | 10 | 2 | US-09-724-961-2 | Sequence 2, Appli |
| 29 | 34 | 100.0 | 10 | 2 | US-09-724-961-3 | Sequence 2, Appli |
| 30 | 34 | 100.0 | 10 | 2 | US-09-724-961-4 | Sequence 4, Appli |
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| 32 | 34 | 100.0 | 10 | 2 | US-09-795-847B-64 | Sequence 64, Appli |
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| 34 | 34 | 100.0 | 10 | 2 | US-09-580-018-3 | Sequence 3, Appli |
| 35 | 34 | 100.0 | 10 | 2 | US-09-580-018-4 | Sequence 4, Appli |
| 36 | 34 | 100.0 | 10 | 2 | US-09-580-018-5 | Sequence 5, Appli |
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| 38 | 34 | 100.0 | 10 | 2 | US-09-724-551-3 | Sequence 3, Appli |
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| 43 | 34 | 100.0 | 10 | 2 | US-09-548-366F-64 | Sequence 64, Appli |
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| 45 | 34 | 100.0 | 10 | 2 | US-09-668-314C-64 | Sequence 64, Appli |

## ALIGNMENTS

RESULT 1
US-09-548-372D-67
; Sequence 67, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Peptide
US-09-548-372D-67

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Best Local Similarity   100.0%;
Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVKMDAE 7
              |||||||
Db          1 EVKMDAE 7

RESULT 2
US-09-548-367D-67
; Sequence 67, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/62801H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-794-927-67

Qy     1  EVKMDAE  7
          |||||||
Db     1  EVKMDAE  7

Query Match          100.0%;  Score 34;  DB 3;  Length 8;
Best Local Similarity 100.0%;  Pred. No. 1.7e+06;
Matches 7;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

RESULT 3
US-09-795-847-67
; Sequence 67, Application US/09795847
; Patent No. US20010018208A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 2834/6280DE
; CURRENT APPLICATION NUMBER: US/09/795,847
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-795-847-67

Qy     1  EVKMDAE  7
          |||||||
Db     1  EVKMDAE  7

Query Match          100.0%;  Score 34;  DB 3;  Length 8;
Best Local Similarity 100.0%;  Pred. No. 1.7e+06;
Matches 7;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

RESULT 4
US-09-794-743-67
; Sequence 67, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 2834/6280BC
; CURRENT APPLICATION NUMBER: US/09/794,743
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-794-743-67

Qy     1  EVKMDAE  7
          |||||||
Db     1  EVKMDAE  7

Query Match          100.0%;  Score 34;  DB 3;  Length 8;
Best Local Similarity 100.0%;  Pred. No. 1.7e+06;
Matches 7;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

RESULT 5
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; Sequence 67, Application US/09794748
; Patent No. US20020037315A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 2834/6280JL
; CURRENT APPLICATION NUMBER: US/09/794,748
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0

OM protein - protein search, using sw model

GenCore version 5.1.7
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Run on: March 15, 2006, 20:18:47 ; Search time 120 Seconds
(without alignments)
24.373 Million cell updates/sec

Title: US-10-721-297-1
Perfect score: 34
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Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 34 | 100.0 | 8 | 3 | US-09-794-927-67 | Sequence 67, Appl |
| 3 | 34 | 100.0 | 8 | 3 | US-09-795-847-67 | Sequence 67, Appl |
| 4 | 34 | 100.0 | 8 | 3 | US-09-794-743-67 | Sequence 67, Appl |
| 5 | 34 | 100.0 | 8 | 3 | US-09-794-748-67 | Sequence 67, Appl |
| 6 | 34 | 100.0 | 8 | 3 | US-09-794-925-67 | Sequence 67, Appl |
| 7 | 34 | 100.0 | 8 | 3 | US-09-681-442-67 | Sequence 67, Appl |
| 8 | 34 | 100.0 | 8 | 3 | US-09-869-414-67 | Sequence 67, Appl |
| 9 | 34 | 100.0 | 8 | 4 | US-10-427-208-52 | Sequence 52, Appl |
| 10 | 34 | 100.0 | 8 | 4 | US-10-652-927-67 | Sequence 67, Appl |
| 11 | 34 | 100.0 | 8 | 4 | US-10-652-830-67 | Sequence 67, Appl |
| 12 | 34 | 100.0 | 8 | 4 | US-10-652-045-67 | Sequence 67, Appl |
| 13 | 34 | 100.0 | 8 | 5 | US-10-476-935-67 | Sequence 67, Appl |
| 14 | 34 | 100.0 | 8 | 5 | US-10-477-076-67 | Sequence 67, Appl |
| 15 | 34 | 100.0 | 8 | 5 | US-10-625-854-196 | Sequence 196, App |
| 16 | 34 | 100.0 | 8 | 5 | US-10-625-854-208 | Sequence 208, App |
| 17 | 34 | 100.0 | 8 | 5 | US-10-817-979-70 | Sequence 70, Appl |
| 18 | 34 | 100.0 | 8 | 6 | US-10-016-717-6 | Sequence 6, Appli |
| 19 | 34 | 100.0 | 4 | 6 | US-10-066-319-3 | Sequence 3, Appli |
| 20 | 34 | 100.0 | 5 | 5 | US-10-625-854-197 | Sequence 197, App |
| 21 | 34 | 100.0 | 5 | 5 | US-10-625-854-209 | Sequence 209, App |
| 22 | 34 | 100.0 | 5 | 5 | US-10-625-854-220 | Sequence 220, App |
| 23 | 34 | 100.0 | 5 | 6 | US-11-090-866-82 | Sequence 82, Appl |
| 24 | 34 | 100.0 | 6 | 6 | US-11-089-918-82 | Sequence 82, Appl |
| 25 | 34 | 100.0 | 6 | 6 | US-11-069-377-82 | Sequence 82, Appl |
| 26 | 34 | 100.0 | 6 | 6 | US-11-090-872-82 | Sequence 82, Appl |
| 27 | 34 | 100.0 | 6 | 6 | US-11-090-399-82 | Sequence 82, Appl |
| 28 | 34 | 100.0 | 10 | 3 | US-09-794-927-64 | Sequence 64, Appl |
| 29 | 34 | 100.0 | 10 | 3 | US-09-795-847-64 | Sequence 64, Appl |
| 30 | 34 | 100.0 | 10 | 3 | US-09-794-743-64 | Sequence 64, Appl |
| 31 | 34 | 100.0 | 10 | 3 | US-09-794-748-64 | Sequence 64, Appl |
| 32 | 34 | 100.0 | 10 | 3 | US-09-796-264-4 | Sequence 4, Appli |
| 33 | 34 | 100.0 | 10 | 3 | US-09-794-925-64 | Sequence 64, Appl |
| 34 | 34 | 100.0 | 10 | 3 | US-09-681-442-64 | Sequence 64, Appl |
| 35 | 34 | 100.0 | 10 | 3 | US-09-845-226-4 | Sequence 4, Appli |
| 36 | 34 | 100.0 | 10 | 3 | US-09-795-903A-4 | Sequence 4, Appli |
| 37 | 34 | 100.0 | 10 | 3 | US-09-908-943A-20 | Sequence 20, Appl |
| 38 | 34 | 100.0 | 10 | 3 | US-09-869-414-64 | Sequence 64, Appl |
| 39 | 34 | 100.0 | 10 | 3 | US-09-548-366-64 | Sequence 64, Appl |
| 40 | 34 | 100.0 | 10 | 4 | US-10-032-818-7 | Sequence 7, Appli |
| 41 | 34 | 100.0 | 10 | 4 | US-10-427-208-53 | Sequence 53, Appl |
| 42 | 34 | 100.0 | 10 | 4 | US-10-652-927-64 | Sequence 64, Appl |
| 43 | 34 | 100.0 | 10 | 4 | US-10-652-830-64 | Sequence 64, Appl |
| 44 | 34 | 100.0 | 10 | 4 | US-10-281-092-12 | Sequence 12, Appl |
| 45 | 34 | 100.0 | 10 | 4 | US-10-652-045-64 | Sequence 64, Appl |

ALIGNMENTS

RESULT 1
US-10-625-854-195

; Sequence 195, Application US/10625854
; Publication No. US20050175626A1
; GENERAL INFORMATION:
; APPLICANT: Delacourte, Andr
; APPLICANT: Sergeant, Nicolas
; TITLE OF INVENTION: Prevention, treatment and diagnosis of diseases associated with
; TITLE OF INVENTION: beta-amyloid formation and/or aggregation
; FILE REFERENCE: 11362.0039.NPUS01
; CURRENT APPLICATION NUMBER: US/10/625,854
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: European Patent Application No. 02447147.6
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/401,497
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 261
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 195
; LENGTH: 7
; TYPE: PRT
; ORGANISM: homo sapiens

US-10-625-854-195

Query Match 100.0%; Score 34; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy    1 EVKMDAE 7
        |||||||
Db    1 EVKMDAE 7

RESULT 2
US-09-794-927-67

; Sequence 67, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 2841/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901

```
CC  (I) has neuroprotective and nootropic activities, and can be used in gene
CC  therapy. (I) can be used for producing preparations of homogenously
CC  processed BACE that may be used for e.g. studying or treating diseases
CC  such as Alzheimer's disease or Down's syndrome. The human BACE1 gene is
CC  located on chromosome 11, more specifically to 11q23.2-23.3. The present
CC  sequence represents a human BACE1 autoproteolysis site amino acid
CC  sequence, which is used in the exemplification of the present invention.
XX
SQ  Sequence 7 AA;

Qy  1 EVNLDAE 7
      |||||||
Db  1 EVNLDAE 7

Query Match            100.0%;  Score 34;  DB 8;  Length 7;
Best Local Similarity  100.0%;  Pred. No. 2e+06;
Matches   7;  Conservative  0;  Mismatches  0;  Indels   0;  Gaps   0;
```

```
RESULT 2
AEA23394
ID  AEA23394 standard; peptide; 7 AA.
XX
AC  AEA23394;
XX
DT  28-JUL-2005  (first entry)
XX
DE  Human APP beta-secretase cleavage site mutant peptide #2.
XX
KW  Screening; beta-amyloid; amyloid precursor protein; neuroprotective;
KW  nootropic; degeneration; neurological disease; beta-secretase; mutein.
XX
OS  Homo sapiens.
OS  Synthetic.
XX
PN  US2005112696-A1.
XX
PD  26-MAY-2005.
XX
PF  25-NOV-2003; 2003US-00721297.
XX
PR  25-NOV-2003; 2003US-00721297.
XX
PA  (UYTE-) UNIV TEXAS SOUTHWESTERN MEDICAL CENT DAL.
XX
PA  Sudhof TC, Li Q;
XX
DR  WPI; 2005-403362/41.
XX
PT  Identifying agents modulating cleavage of amyloid beta-precursor protein
PT  by beta-secretase, by contacting chimeric molecule comprising cleavage
PT  site with beta-secretase in presence of modulating agent, measuring
PT  nuclear localization.
XX
PS  Claim 3; Page 10; 20pp; English.
XX
CC  The present invention relates to a method of screening and identifying
CC  agents that modulate cleavage of amyloid beta-precursor protein (APP) or
CC  APP-like proteins such as APLP1 and APLP2 by a beta-secretase. The method
CC  involves contacting a chimeric molecule comprising a transmembrane region
CC  (TMR) with a gamma- or beta-secretase cleavage site and an APP C-
CC  terminal cytoplasmic tail modified with beta-secretase in presence and
CC  absence of a modulating agent and identifying cleavage by measuring
CC  nuclear localization of C-terminal cytoplasmic tail. The invention is
CC  useful in the treatment of Alzheimer's disease. The present sequence is
CC  the human APP beta-secretase cleavage site peptide containing swedish
CC  mutation.
XX
SQ  Sequence 7 AA;

Qy  1 EVNLDAE 7
      |||||||
Db  1 EVNLDAE 7

Query Match            100.0%;  Score 34;  DB 9;  Length 7;
Best Local Similarity  100.0%;  Pred. No. 2e+06;
Matches   7;  Conservative  0;  Mismatches  0;  Indels   0;  Gaps   0;
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```
RESULT 3
AEB09785
ID  AEB09785 standard; peptide; 7 AA.
XX
AC  AEB09785;
XX
DT  08-SEP-2005  (first entry)
XX
DE  Autoproteolysis sequence for engineered BACE1, SEQ ID 21.
XX
KW  Protein engineering; Beta secretase; amyloid precursor protein;
KW  Alzheimers disease; Down syndrome; neuroprotective; nootropic;
KW  autoproteolytic site.
XX
OS  Homo sapiens.
XX
PN  WO2005060384-A2.
XX
PD  07-JUL-2005.
XX
PF  07-JUL-2005.
XX
PR  02-DEC-2003; 2003US-00726967.
XX
PA  (SUNE-) SUNESIS PHARM INC.
XX
PA  Ballinger M, Randal ML;
XX
DR  WPI; 2005-497666/50.
XX
PT  New polypeptide having beta site amyloid precursor protein APP-cleaving
PT  enzyme (BACE) activity, having a prodomain, and autoproteolysis site and
PT  protease domain, for producing preparations of homogeneously processed
PT  BACE.
XX
PS  Claim 12; SEQ ID NO 21; 71pp; English.
XX
CC  The invention relates to a polypeptide (I) comprising in order from N-
CC  terminus to C-terminus, a prodomain (comprising at least six contiguous
CC  amino acids of AEB09767), an autoproteolysis site and a protease domain
CC  (comprising at least one amino acid sequence chosen from a sequence at
CC  least 90% identical to residues 74-207, 241-361 or 389-446 of AEB09765),
CC  where the polypeptide is capable of being cleaved at the autoproteolysis
CC  site, to thus release a free protease domain that has beta site amyloid
CC  precursor protein (APP)-cleaving enzyme (BACE, beta secretase) activity.
CC  Also included are a nucleic acid sequence encoding the polypeptide, a
CC  vector for expressing the polypeptide and a host cell expressing the
CC  polypeptide. The polypeptide is useful for producing amyloid precursor protein
CC  homogeneously processed BACE, and for cleaving Abeta peptide, where the cerebral
CC  deposition of Abeta peptide causes Alzheimer's disease and Down's
CC  syndrome. The polypeptide comprises a prodomain, an engineered cleavage
CC  site, and a protease domain. The polypeptide is properly folded and is
CC  cleaved at the engineered cleavage site in vitro, to produce homogenous
CC  preparations of purified protease having BACE activity. The present
CC  sequence is an autoproteolytic cleavage site which may be engineered into
CC  the polypeptide of the invention.
XX
SQ  Sequence 7 AA;

Qy  1 EVNLDAE 7
      |||||||
Db  1 EVNLDAE 7

Query Match            100.0%;  Score 34;  DB 9;  Length 7;
Best Local Similarity  100.0%;  Pred. No. 2e+06;
Matches   7;  Conservative  0;  Mismatches  0;  Indels   0;  Gaps   0;
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OM protein - protein search, using sw model

GenCore version 5.1.7
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Run on:　March 15, 2006, 20:07:46 ; Search time 135 seconds
(without alignments)
22.783 Million cell updates/sec

Title:　　　　US-10-721-297-10
Perfect score:　34
Sequence:　　1 EVNLDAE 7
Scoring table:　BLOSUM62
　　　　　　　Gapop 10.0 , Gapext 0.5
Searched:　　2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters:　2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :　A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | % Query Match | Length | DB ID | Description |
|---|---|---|---|---|---|
| 1 | 34 | 100.0 | 7 | ADP83933 | Human BAC |
| 2 | 34 | 100.0 | 7 | AEA23394 | Human APP |
| 3 | 34 | 100.0 | 7 | Aeb09785 | Autoprote |
| 4 | 34 | 100.0 | 8 | Aay94771 | Beta-secr |
| 5 | 34 | 100.0 | 8 | Aae10661 | Human asp |
| 6 | 34 | 100.0 | 8 | Aae02613 | Human Asp |
| 7 | 34 | 100.0 | 8 | Abb78622 | Human bet |
| 8 | 34 | 100.0 | 8 | Abr54159 | Beta-secr |
| 9 | 34 | 100.0 | 8 | Aea23385 | Human APP |
| 10 | 34 | 100.0 | 9 | Aaw82081 | Fluorogen |
| 11 | 34 | 100.0 | 9 | Aab07874 | A peptide |
| 12 | 34 | 100.0 | 9 | Aab07894 | Substrate |
| 13 | 34 | 100.0 | 9 | Aag73297 | Protease |
| 14 | 34 | 100.0 | 9 | Abb06519 | Beta-secr |
| 15 | 34 | 100.0 | 9 | Abb09003 | Peptide # |
| 16 | 34 | 100.0 | 9 | Abu60429 | Protease |
| 17 | 34 | 100.0 | 9 | Abu60441 | Protease |
| 18 | 34 | 100.0 | 9 | Aae16663 | Oligopept |
| 19 | 34 | 100.0 | 9 | Aau74837 | Synthetic |
| 20 | 34 | 100.0 | 9 | Abb07598 | Synthetic |
| 21 | 34 | 100.0 | 9 | Aam50897 | Oligopept |
| 22 | 34 | 100.0 | 9 | Abp97975 | Oligopept |
| 23 | 34 | 100.0 | 9 | Abp57515 | Different |
| 24 | 34 | 100.0 | 9 | Abp57084 | Synthetic |
| 25 | 34 | 100.0 | 9 | Abp71468 | Beta-secr |
| 26 | 34 | 100.0 | 9 | Aao16449 | Beta-secr |
| 27 | 34 | 100.0 | 9 | Abp71269 | Oligopep |
| 28 | 34 | 100.0 | 9 | Abr44377 | Oligonpep |
| 29 | 34 | 100.0 | 9 | Abp58375 | Beta-secr |
| 30 | 34 | 100.0 | 9 | Aao26801 | Beta-secr |
| 31 | 34 | 100.0 | 9 | Abg75940 | Synthetic |
| 32 | 34 | 100.0 | 9 | Abp71630 | Beta-secr |
| 33 | 34 | 100.0 | 9 | Aae36000 | APP subst |
| 34 | 34 | 100.0 | 9 | Abr82372 | Beta-secr |
| 35 | 34 | 100.0 | 9 | Abr56258 | Amyloid P |
| 36 | 34 | 100.0 | 9 | Abr62018 | Beta-secr |
| 37 | 34 | 100.0 | 9 | Abr61887 | Beta-secr |
| 38 | 34 | 100.0 | 9 | Abr56195 | Amyloid p |
| 39 | 34 | 100.0 | 9 | Adc29723 | Synthetic |
| 40 | 34 | 100.0 | 9 | Adc26557 | Beta-secr |
| 41 | 34 | 100.0 | 9 | Adc10532 | Synthetic |
| 42 | 34 | 100.0 | 9 | Add80769 | Synthetic |
| 43 | 34 | 100.0 | 9 | Adg91228 | Synthetic |
| 44 | 34 | 100.0 | 9 | Adj47996 | Human BAC |
| 45 | 34 | 100.0 | 9 | Adm16649 | Oligopep |

## ALIGNMENTS

RESULT 1
ADP83933
ID   ADP83933 standard; peptide; 7 AA.
XX
AC   ADP83933;
XX
DT   23-SEP-2004  (first entry)
XX
DE   Human BACE1 autoproteolysis site SEQ ID NO:59.
XX
KW   human; beta-site amyloid precursor protein cleaving enzyme 1;
KW   beta-site APP cleaving enzyme 1; BACE1; BACE1 isoform A; prodomain;
KW   engineered cleavage site; protease domain; neuroprotective; nootropic;
KW   gene therapy; Alzheimer's disease; Down's syndrome.
XX
OS   Homo sapiens.
XX
PN   WO2004056962-A2.
XX
PD   08-JUL-2004.
XX
PF   02-DEC-2003; 2003WO-US038314.
XX
PR   04-DEC-2002; 2002US-0430984P.
XX
PA   (SUNE-) SUNESIS PHARM INC.
XX
PI   Ballinger M;
XX
DR   WPI; 2004-507703/48.
XX
PT   New polypeptides for producing homogenously processed preparations of
PT   beta site amyloid precursor protein-cleaving enzyme comprises a
PT   prodomain, an engineered cleavage site and a protease domain.
XX
PS   Claim 10; SEQ ID NO 59; 40pp; English.
XX
CC   The present invention describes a polypeptide (I) comprising in order
CC   from the N-terminus to the C-terminus: (a) a prodomain comprising at
CC   least 6 contiguous amino acids of the 16 amino acid sequence of SEQ ID
CC   NO:3 (ADP83877, comprising residues 22-37 of SEQ ID NO:1 (ADP83876) which
CC   is the longest isoform of human beta-site amyloid precursor protein (APP)
CC   cleaving enzyme 1 (BACE1), isoform A); (b) an engineered cleavage site;
CC   and (c) a protease domain. (I) is capable of being cleaved at the
CC   engineered cleavage site, and so releases a free protease domain that has
CC   BACE1 activity. Also described: (1) a nucleic acid sequence encoding (I);
CC   (2) a vector for expression of (I); and (3) a host cell expressing (I).

RESULT 3
H86169
hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: H86169
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.R.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.;
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.;
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-672 <STO>
A;Cross-references: UNIPROT:Q92WB1; UNIPARC:UPI00000A0A6A; GB:AE005172; NID:g94204304; PI
C;Genetics:
A;Map position: 1

Query Match      91.2%;    Score 31;  DB 2;  Length 672;
Best Local Similarity    85.7%;    Pred. No. 61;
Matches    6;  Conservative  1;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 EVNLDAE 7
        |||||:|
Db  538 EVNLDSE 544


RESULT 4
T18655
hypothetical protein B0035.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18655
R;White, S.
submitted to the EMBL Data Library, May 1996
A;Reference number: Z19002
A;Accession: T18655
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-126 <WIL>
A;Cross-references: UNIPROT:Q17435; UNIPARC:UPI000013I727; EMBL:Z73102; PIDN:CAA97410.1;
A;Experimental source: clone B0035
C;Genetics:
A;Gene: CESP:B0035.4
A;Map position: 4
A;Introns: 29/3; 73/3
C;Superfamily: Arabidopsis thaliana hypothetical protein P22013.29

Query Match      88.2%;    Score 30;  DB 2;  Length 126;
Best Local Similarity    71.4%;    Pred. No. 16;
Matches    5;  Conservative  2;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 EVNLDAE 7
        ||:||||
Db  119 QINLDAE 125


RESULT 5
A72411
hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: A72411
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: A72411
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-278 <ARN>
A;Cross-references: UNIPROT:Q9WW10; UNIPARC:UPI00000C146F; GB:AE001701; GB:AE000512; NID:
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM0163

Query Match      88.2%;    Score 30;  DB 2;  Length 278;
Best Local Similarity    85.7%;    Pred. No. 38;
Matches    6;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy    1 EVNLDAE 7
        |||||:|
Db  241 EVNLDVE 247


RESULT 6
C81672
serine hydroxymethyltransferase TC0716 [imported] - Chlamydia muridarum (strain Nigg)
C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: C81672
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: C81672
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-497 <TET>
A;Cross-references: UNIPROT:Q9PJW0; UNIPARC:UPI00000057A25; GB:AE002340; GB:AE002160; NII
A;Experimental source: strain Nigg (MoPn)
C;Genetics:
A;Gene: TC0716
C;Superfamily: serine/glycine hydroxymethyltransferase

Query Match      88.2%;    Score 30;  DB 2;  Length 497;
Best Local Similarity    85.7%;    Pred. No. 74;
Matches    6;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy    1 EVNLDAE 7
        |||||:|
Db  202 EVNLDTE 208


RESULT 7
H71516
glycine hydroxymethyltransferase (EC 2.1.2.1) - Chlamydia trachomatis (serotype D, strai
N;Alternate names: serine hydroxymethyltransferase
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C;Accession: H71516
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac
A;Reference number: A71570; MUID:99008809; PMID:9784136
A;Accession: H71516
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-497 <ARN>
A;Cross-references: UNIPROT:O84439; UNIPARC:UPI00012B85B; GB:AE001316; GB:AE001273; NID:
A;Experimental source: serotype D, strain UW-3/Cx
C;Genetics:
A;Gene: glyA
C;Superfamily: serine/glycine hydroxymethyltransferase

GenCore version 5.1.7

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OM protein - protein search, using sw model

Run on:    March 15, 2006, 20:13:01 ; Search time 24 Seconds
                                28.063 Million cell updates/sec
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    PIR_80:*
              1: pir1:*
              2: pir2:*
              3: pir3:*
              4: pir4:*

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Sequence:    1 EVNLDAE 7
Perfect score:    34
Title:    34

Searched:    283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:    283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 34 | 100.0 | 419 | 2 | D42725 | nitrile hydratase |
| 2 | 31 | 91.2 | 368 | 2 | A28825 | keratin, type I no |
| 3 | 31 | 91.2 | 672 | 2 | H86169 | hypothetical prote |
| 4 | 30 | 88.2 | 126 | 2 | T16655 | hypothetical prote |
| 5 | 30 | 88.2 | 278 | 2 | A72411 | hypothetical prote |
| 6 | 30 | 88.2 | 497 | 2 | C81672 | serine hydroxymeth |
| 7 | 30 | 88.2 | 497 | 2 | H71516 | glycine hydroxymet |
| 8 | 30 | 88.2 | 802 | 2 | C90326 | hypothetical prote |
| 9 | 30 | 88.2 | 282 | 2 | T26112 | hypothetical prote |
| 10 | 29 | 85.3 | 289 | 2 | D69795 | transcription regu |
| 11 | 29 | 85.3 | 295 | 2 | F83867 | dihydrodipicolinat |
| 12 | 29 | 85.3 | 326 | 2 | A83087 | conserved hypothet |
| 13 | 29 | 85.3 | 340 | 2 | T35558 | DNA-directed RNA p |
| 14 | 29 | 85.3 | 394 | 2 | F69888 | alanine racemase h |
| 15 | 29 | 85.3 | 400 | 2 | E95099 | 30S ribosomal prot |
| 16 | 29 | 85.3 | 400 | 2 | D97967 | ribosomal protein |
| 17 | 29 | 85.3 | 434 | 2 | D88305 | protein R03D7.4 [i |
| 18 | 29 | 85.3 | 434 | 2 | S72430 | transcription elon |
| 19 | 29 | 85.3 | 442 | 2 | B82633 | nitrile hydratase |
| 20 | 29 | 85.3 | 470 | 2 | C75591 | threonine synthase |
| 21 | 29 | 85.3 | 508 | 2 | B96658 | hypothetical prote |
| 22 | 29 | 85.3 | 550 | 2 | AD3494 | oligopeptide trans |
| 23 | 29 | 85.3 | 619 | 1 | JH0776 | hydrogenase (EC 1. |
| 24 | 29 | 85.3 | 712 | 2 | AB2776 | DNA gyrase subunit |
| 25 | 29 | 85.3 | 712 | 2 | H97555 | DNA gyrase chain b |
| 26 | 29 | 85.3 | 743 | 2 | D64062 | GTP diphosphokinas |
| 27 | 29 | 85.3 | 929 | 2 | T52517 | hypothetical prote |
| 28 | 28 | 82.4 | 1331 | 2 | H82211 | sensory box sensor |
| 29 | 28 | 82.4 | 161 | 1 | G64814 | molybdenum cofacto |
| 30 | 28 | 82.4 | 161 | 2 | P85586 | molybdopterin bios |
| 31 | 28 | 82.4 | 161 | 2 | E90736 | molybdenum cofacto |
| 32 | 28 | 82.4 | 197 | 2 | S61047 | hypothetical prote |
| 33 | 28 | 82.4 | 201 | 2 | E84412 | hypothetical prote |
| 34 | 28 | 82.4 | 353 | 2 | A95998 | probable sugar upt |
| 35 | 28 | 82.4 | 418 | 2 | S56369 | hypothetical prote |
| 36 | 28 | 82.4 | 418 | 2 | H86109 | probable transport |
| 37 | 28 | 82.4 | 418 | 2 | HQ2JUL | probable transport |
| 38 | 28 | 82.4 | 459 | 2 | B98269 | hypothetical prote |
| 39 | 28 | 82.4 | 509 | 2 | S76122 | phosphoglycerate d |
| 40 | 28 | 82.4 | 533 | 2 | D64435 | hypothetical prote |
| 41 | 28 | 82.4 | 538 | 2 | T31002 | hydrogenase (EC 1. |
| 42 | 28 | 82.4 | 596 | 1 | AG3295 | hypothetical prote |
| 43 | 28 | 82.4 | 597 | 2 | B82881 | hypothetical prote |
| 44 | 28 | 82.4 | 809 | 2 | S67665 | ubiquitin-specific |
| 45 | 28 | 82.4 | 970 | 2 | C84488 | hypothetical prote |

ALIGNMENTS

RESULT 1
D42725
nitrile hydratase region 3'-hypothetical protein P47K - Pseudomonas chlororaphis
C;Species: Pseudomonas chlororaphis
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004
C;Accession: D42725
R;Nishiyama, M.; Horinouchi, S.; Kobayashi, M.; Nagasawa, T.; Yamada, H.; Beppu, T.
J. Bacteriol. 173, 2465-2472, 1991
A;Title: Cloning and characterization of genes responsible for metabolism of nitrile co
A;Reference number: A42725; MUID:91193202; PMID:2013568
A;Accession: D42725
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-419 <NIS>
A;Cross-references: UNIPROT:P31521; UNIPARC:UPI000013102A; GB:D90216; NID:g216850; PIDN:(
C;Superfamily: conserved hypothetical protein yciC

Query Match        100.0%;  Score 34;  DB 2;  Length 419;
Best Local Similarity   100.0%;
Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 EVNLDAE 7
           |||||||
Db      48 EVNLDAE 54

RESULT 2
A28825
keratin, type I nonepidermal - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: A28825
R;LaFlamme, S. E.; Jamrich, M.; Richter, K.; Sargent, T. D.; Dawid, I. B.
Genes Dev. 2, 853-862, 1988
A;Title: Xenopus endo B is a keratin preferentially expressed in the embryonic notochor
A;Reference number: A28825; MUID:89092007; PMID:2463213
A;Accession: A28825
A;Molecule type: mRNA
A;Residues: 1-368 <LAF>
A;Cross-references: UNIPROT:P08802; UNIPARC:UPI00012DAEC; GB:Y00230; NID:g64863; PIDN:(
C;Genetics:
A;Start codon: GGT
C;Superfamily: cytoskeletal keratin
C;Keywords: coiled coil

Query Match        91.2%;  Score 31;  DB 2;  Length 368;
Best Local Similarity   85.7%;
Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 EVNLDAE 7
           ||||| |
Db     219 QVNLDAE 225

DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Transcription factor protein.
GN   Name=Ci-ATF3;
OS   Ciona intestinalis.
OC   Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC   Phlebobranchia; Cionidae; Ciona.
OX   NCBI_TaxID=7719;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15269171; DOI=10.1242/dev.01270;
RA   Imai K.S., Hino K., Yagi K., Satoh N., Satou Y.;
RT   "Genomewide surveys of developmentally relevant genes in Ciona
RT   intestinalis.";
RL   Development 131:4047-4058(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=12736827; DOI=10.1007/s00427-003-0330-z;
RA   Satou Y., Satoh N.;
RT   "Genomewide surveys of developmentally relevant genes in Ciona
RT   intestinalis.";
RL   Dev. Genes Evol. 213:211-212(2003).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Satou Y.;
RT   "Expressed genes in Ciona intestinalis.";
RL   Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB210313; BAE06318.1; -; mRNA.
SQ   SEQUENCE 273 AA; 31974 MW; 4DD5C47C49B77361 CRC64;

Qy      1 EVNLDAE 7
          |:|||||
Db    217 EVNLDAE 223

Query Match             97.1%;  Score 33;  DB 2;  Length 273;
Best Local Similarity   85.7%;  Pred. No. 67;
Matches     6;  Conservative  1;  Mismatches  0;  Indels  0;  Gaps  0;

RESULT 3
ID   Q6N9S6_RHOPA
AC   Q6N9S6;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=RPA1462;
OS   Rhodopseudomonas palustris.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Bradyrhizobiaceae; Rhodopseudomonas.
OX   NCBI_TaxID=1076;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CGA009 / ATCC BAA-98;
RX   PubMed=14704707; DOI=10.1038/nbt923;
RA   Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
RA   Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
RA   Gibson J.L., Hanson T.E., Bobst C., Torres Y Torres J.L., Peres C.,
RA   Harrison F.H., Gibson J., Harwood C.S.;
RT   "Complete genome sequence of the metabolically versatile
RT   photosynthetic bacterium Rhodopseudomonas palustris.";
RL   Nat. Biotechnol. 22:55-61(2004).
DR   EMBL; BX572597; CAE26904.1; -; Genomic_DNA.
DR   InterPro; IPR003495; CobW.
DR   InterPro; IPR011629; CobW_C.
DR   Pfam; PF02492; cobW; 1.
DR   Pfam; PF07683; CobW_C; 1.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE 402 AA; 45220 MW; 6D5A4AB18877791B CRC64;

Query Match             94.1%;  Score 32;  DB 2;  Length 402;
Best Local Similarity   85.7%;  Pred. No. 1.7e+02;

Matches     6;  Conservative  1;  Mismatches  0;  Indels  0;  Gaps  0;

Qy      1 EVNLDAE 7
          |||:|||
Db     44 EVNLDAE 50

RESULT 4
ID   Q8PYH8_METMA
AC   Q8PYH8;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Conserved protein.
GN   OrderedLocusNames=MM0884;
OS   Methanosarcina mazei (Methanosarcina frisia).
OC   Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC   Methanosarcinaceae; Methanosarcina.
OX   NCBI_TaxID=2209;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Goe1 / Go1 / ATCC BAA-199 / DSM 3647 / OCM 88;
RX   MEDLINE=22120827; PubMed=12125824;
RA   Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
RA   Martinez-Arias R., Henne A., Wiezer A., Baeumer S., Jacobi C.,
RA   Brueggemann H., Lienard T., Christmann A., Boemecke M., Steckel S.,
RA   Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
RA   Fritz H.-J., Gottschalk G.;
RT   "The genome of Methanosarcina mazei: evidence for lateral gene
RT   transfer between Bacteria and Archaea.";
RL   J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
DR   EMBL; AE013314; AAM30580.1; -; Genomic_DNA.
KW   Complete proteome.
SQ   SEQUENCE 84 AA; 9519 MW; F78DECBDED67B266 CRC64;

Qy      1 EVNLDAE 7
          |:|:|||
Db     78 EINLDAE 84

Query Match             91.2%;  Score 31;  DB 2;  Length 84;
Best Local Similarity   71.4%;  Pred. No. 55;
Matches     5;  Conservative  2;  Mismatches  0;  Indels  0;  Gaps  0;

RESULT 5
ID   Q8TIW2_METAC
AC   Q8TIW2;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Predicted protein.
GN   OrderedLocusNames=MA4028;
OS   Methanosarcina acetivorans.
OC   Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC   Methanosarcinaceae; Methanosarcina.
OX   NCBI_TaxID=2214;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C2A / ATCC 35395 / DSM 2834;
RX   MEDLINE=21929760; PubMed=11932238; DOI=10.1101/gr.223902;
RA   Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA   FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA   Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,
RA   Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA   Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA   Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,
RA   Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA   Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA   Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.T.,
RA   Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA   Metcalf W.W., Birren B.;

OM protein - protein search, using sw model

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GenCore version 5.1.7

Run on:         March 15, 2006, 20:08:12 ; Search time 146.5 Seconds
                (without alignments)
                33.711 Million cell updates/sec

Title:          US-10-721-297-10
Perfect score:  34
Sequence:       1 EVNLDAE 7

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters:    2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      UniProt_05.80:*
                1:   uniprot_sprot:*
                2:   uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 34 | 100.0 | 419 | 1 | P47K_PSECL | P31521 pseudomonas |
| 2 | 33 | 97.1 | 273 | 2 | Q4H3V9_CIOIN | Q4h3v9 ciona intes |
| 3 | 32 | 94.1 | 402 | 2 | Q6N9S6_RHOPA | Q6n9s6 rhodopseudo |
| 4 | 31 | 91.2 | 84 | 2 | Q8PYH8_METMA | Q8pyh8 methanosarc |
| 5 | 31 | 91.2 | 84 | 2 | Q8TIW2_METAC | Q8tiw2 methanosarc |
| 6 | 31 | 91.2 | 118 | 2 | Q4RZZ2_TETNG | Q4rzz2 tetraodon n |
| 7 | 31 | 91.2 | 221 | 2 | Q82WI7_NITEU | Q82wi7 nitrosomona |
| 8 | 31 | 91.2 | 226 | 2 | Q8TP55_METAC | Q8tp55 methanosarc |
| 9 | 31 | 91.2 | 281 | 2 | Q8A4M0_BACTN | Q8a4m0 bacteroides |
| 10 | 31 | 91.2 | 368 | 1 | K1C18_XENLA | P08802 xenopus lae |
| 11 | 31 | 91.2 | 402 | 2 | Q6FBU8_ACIAD | Q6fbu8 acinetobact |
| 12 | 31 | 91.2 | 408 | 2 | Q5NG56_FRATT | Q5ng56 francisella |
| 13 | 31 | 91.2 | 428 | 2 | Q6INH6_XENLA | Q6inh6 xenopus lae |
| 14 | 31 | 91.2 | 436 | 2 | Q8AVI2_XENLA | Q8avi2 xenopus lae |
| 15 | 31 | 91.2 | 672 | 2 | Q92WB1_ARATH | Q92wb1 arabidopsis |
| 16 | 31 | 91.2 | 1154 | 2 | Q6MEZ0_PARUW | Q6mez0 parachlamyd |
| 17 | 31 | 91.2 | 1186 | 2 | Q522M9_MAGGR | Q522m9 magnaporthe |
| 18 | 30 | 88.2 | 54 | 2 | Q8P193_STRP8 | Q8p193 streptococc |
| 19 | 30 | 88.2 | 126 | 1 | PFD4_CAEEL | Q17435 caenorhabdi |
| 20 | 30 | 88.2 | 126 | 2 | Q61SQ9_CAEBR | Q61sq9 caenorhabdi |
| 21 | 30 | 88.2 | 142 | 2 | Q602K3_CAEBR | Q602k3 caenorhabdi |
| 22 | 30 | 88.2 | 222 | 2 | Q5BCM3_EMENI | Q5bcm3 aspergillus |
| 23 | 30 | 88.2 | 278 | 2 | Q5CBM4_9THEM | Q5cbm4 thermotoga |
| 24 | 30 | 88.2 | 278 | 2 | Q5CBK6_9THEM | Q5cbk6 thermotoga |
| 25 | 30 | 88.2 | 278 | 2 | Q5CB78_9THEM | Q5cb78 thermotoga |
| 26 | 30 | 88.2 | 278 | 2 | Q9WY10_THEMA | Q9wy10 thermotoga |
| 27 | 30 | 88.2 | 294 | 1 | PHO85_YARLI | PHO85 yarrowia li |
| 28 | 30 | 88.2 | 330 | 1 | PHO85_DEBHA | PHO85 debaryomyce |
| 29 | 30 | 88.2 | 372 | 2 | Q5V641_HALMA | Q5v641 haloarcula |
| 30 | 30 | 88.2 | 497 | 1 | GLYA_CHLMU | Q9pjw0 chlamydia m |
| 31 | 30 | 88.2 | 497 | 1 | GLYA_CHLTR | O84439 chlamydia t |
| 32 | 30 | 88.2 | 802 | 2 | Q97XQ7_SULSO | Q97xq7 sulfolobus |
| 33 | 30 | 88.2 | 926 | 2 | Q5AY24_EMENI | Q5ay24 aspergillus |
| 34 | 30 | 88.2 | 982 | 2 | Q70XJ8_GIALA | Q70xj8 giardia lam |
| 35 | 29 | 85.3 | 81 | 2 | Q6LXG3_METMP | Q6lxg3 methanococc |
| 36 | 29 | 85.3 | 89 | 2 | Q4NFI2_9MICC | Q4nfi2 arthrobacte |
| 37 | 29 | 85.3 | 142 | 2 | Q8R721_THETN | Q8r721 thermoanaer |
| 38 | 29 | 85.3 | 165 | 2 | Q5GU43_XANOR | Q5gu43 xanthomonas |
| 39 | 29 | 85.3 | 173 | 2 | Q87ZB6_PSESM | Q87zb6 pseudomonas |
| 40 | 29 | 85.3 | 202 | 2 | Q6CHM2_YARLI | Q6chm2 yarrowia li |
| 41 | 29 | 85.3 | 212 | 2 | Q4ZRA4_PSESY | Q4zra4 pseudomonas |
| 42 | 29 | 85.3 | 241 | 2 | Q5P619_AZOSE | Q5p619 azoarcus sp |
| 43 | 29 | 85.3 | 242 | 2 | Q649N4_9ARCH | Q649n4 uncultured |
| 44 | 29 | 85.3 | 255 | 2 | Q4QK92_HAEI8 | Q4qk92 haemophilus |
| 45 | 29 | 85.3 | 260 | 2 | Q5E3T6_VIBF1 | Q5e3t6 vibrio fisc |

ALIGNMENTS

RESULT 1

| ID | P47K_PSECL |  | STANDARD; | PRT; | 419 AA. |
|---|---|---|---|---|---|
| AC | P31521; |

DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   47 kDa protein (P47K).
OS   Pseudomonas chlororaphis (Pseudomonas aureofaciens).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=333;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC   STRAIN=B23;
RX   MEDLINE=91193202; PubMed=2013568;
RA   Nishiyama M., Horinouchi S., Kobayashi M., Nagasawa T., Yamada H.,
RA   Beppu T.;
RT   "Cloning and characterization of genes responsible for metabolism of
RT   nitrile compounds from Pseudomonas chlororaphis B23.";
RL   J. Bacteriol. 173:2465-2472(1991).
CC   -!- FUNCTION: The presence of P47K is critical for the expression of
CC       the nitrile hydratase genes. May stabilize or activate the nitrile
CC       hydratase proteins.
CC   --------------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --------------------------------------------------------------------------
DR   EMBL; D90216; BAA14247.1; -; Genomic_DNA.
DR   PIR; D42725; D42725.
DR   HSSP; P24203; 1NIJ.
DR   InterPro; IPR011629; CobW_C.
DR   InterPro; IPR003495; P47K_Cob_synth.
DR   Pfam; PF02492; cobW; 1.
DR   Pfam; PF07683; CobW_C; 1.
SQ   SEQUENCE   419 AA;  46666 MW;  FF5113800E27FF0C CRC64;

| Query Match | 100.0%; | Score 34; | DB 1; | Length 419; |
|---|---|---|---|---|
| Best Local Similarity | 100.0%; |
| Matches | 7; | Conservative | 0; | Mismatches | 0; | Indels | 0; | Gaps | 0; |

Qy              1 EVNLDAE 7
                  |||||||
Db             48 EVNLDAE 54

RESULT 2

| ID | Q4H3V9_CIOIN |  | PRELIMINARY; | PRT; | 273 AA. |
|---|---|---|---|---|---|
| AC | Q4H3V9; |

DT   13-SEP-2005 (TrEMBLrel. 31, Created)

; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,981
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 016865-00030OUS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 219:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-802-981-219

Qy
Db

Query Match                    100.0%;    Score 34;    DB 2;    Length 9;
Best Local Similarity          100.0%;    Pred. No. 4.6e+05;
Matches    7;    Conservative    0;    Mismatches    0;    Indels    0;    Gaps    0;

Qy    1  EVNLDAE  7
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Db    2  EVNLDAE  8

RESULT 3
US-09-724-566A-52
; Sequence 52, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guriqbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52

; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligopeptide substrate

US-09-724-566A-52

Qy
Db

Query Match                    100.0%;    Score 34;    DB 2;    Length 9;
Best Local Similarity          100.0%;    Pred. No. 4.6e+05;
Matches    7;    Conservative    0;    Mismatches    0;    Indels    0;    Gaps    0;

Qy    1  EVNLDAE  7
         |||||||
Db    2  EVNLDAE  8

RESULT 4
US-09-724-566A-83
; Sequence 83, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guriqbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: APP fragment P5-P4'wt

US-09-724-566A-83

Qy
Db

Query Match                    100.0%;    Score 34;    DB 2;    Length 9;
Best Local Similarity          100.0%;    Pred. No. 4.6e+05;
Matches    7;    Conservative    0;    Mismatches    0;    Indels    0;    Gaps    0;

Qy    1  EVNLDAE  7
         |||||||
Db    2  EVNLDAE  8

RESULT 5
US-09-471-669A-52
; Sequence 52, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guriqbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6830918mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael

QM protein - protein search, using sw model

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GenCore version 5.1.7

Run on:    March 15, 2006, 20:17:57 ; Search time 33.5 Seconds
           (without alignments)
           17.276 Million cell updates/sec

Title:          US-10-721-297-10
Perfect score:  34
Sequence:       1 EVNLDAE 7
Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5
Searched:       572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters:     572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : Issued_Patents AA:*
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Match Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 34 | 100.0 | 10 | 2 | US-09-668-314C-71 | Sequence 71, Appl |
| 2 | 34 | 100.0 | 10 | 2 | US-09-802-981-219 | Sequence 219, App |
| 3 | 34 | 100.0 | 10 | 2 | PCT-US94-07043A-3 | Sequence 3, Appli |
| 4 | 34 | 100.0 | 9 | 2 | US-09-724-566A-52 | Sequence 52, Appl |
| 5 | 34 | 100.0 | 9 | 2 | US-09-471-669A-83 | Sequence 83, Appl |
| 6 | 34 | 100.0 | 9 | 2 | US-09-895-843-8 | Sequence 8, Appl |
| 7 | 34 | 100.0 | 9 | 2 | US-10-192-424-8 | Sequence 8, Appli |
| 8 | 34 | 100.0 | 9 | 2 | US-10-171-343-8 | Sequence 8, Appli |
| 9 | 34 | 100.0 | 9 | 2 | US-10-337-075-8 | Sequence 8, Appli |
| 10 | 34 | 100.0 | 9 | 1 | US-08-659-984A-19 | Sequence 19, Appl |
| 11 | 34 | 100.0 | 9 | 2 | US-08-660-531-19 | Sequence 19, Appl |
| 12 | 34 | 100.0 | 9 | 2 | US-09-548-372D-63 | Sequence 19, Appl |
| 13 | 34 | 100.0 | 10 | 2 | US-09-548-367D-63 | Sequence 63, Appl |
| 14 | 34 | 100.0 | 10 | 2 | US-09-551-853D-63 | Sequence 63, Appl |
| 15 | 34 | 100.0 | 10 | 2 | US-09-604-608-5 | Sequence 5, Appli |
| 16 | 34 | 100.0 | 10 | 2 | US-09-416-901B-63 | Sequence 63, Appl |
| 17 | 34 | 100.0 | 10 | 2 | US-09-548-376D-63 | Sequence 63, Appl |
| 18 | 34 | 100.0 | 10 | 2 | US-09-794-927A-63 | Sequence 63, Appl |
| 19 | 34 | 100.0 | 10 | 2 | US-09-548-373D-63 | Sequence 63, Appl |
| 20 | 34 | 100.0 | 10 | 2 | US-09-794-927A-63 | Sequence 63, Appl |
| 21 | 34 | 100.0 | 10 | 2 | US-09-795-847B-63 | Sequence 63, Appl |
| 22 | 34 | 100.0 | 10 | 2 | US-09-869-414-63 | Sequence 63, Appl |
| 23 | 34 | 100.0 | 10 | 2 | US-09-548-366F-63 | Sequence 63, Appl |
| 24 | 34 | 100.0 | 10 | 2 | US-09-548-368D-63 | Sequence 63, Appl |
| 25 | 34 | 100.0 | 10 | 2 | US-09-794-925A-63 | Sequence 63, Appl |
| 26 | 34 | 100.0 | 10 | 2 | US-09-668-314C-63 | Sequence 63, Appl |
| 27 | 34 | 100.0 | 10 | 2 | US-09-404-578-19 | Sequence 19, Appl |
| 28 | 34 | 100.0 | 10 | 2 | US-09-548-365-63 | Sequence 63, Appl |
| 29 | 34 | 100.0 | 10 | 2 | US-09-794-743-63 | Sequence 63, Appl |
| 30 | 34 | 100.0 | 11 | 4 | PCT-US94-07043A-3 | Sequence 3, Appli |
| 31 | 34 | 100.0 | 12 | 2 | US-09-895-843-1 | Sequence 1, Appli |
| 32 | 34 | 100.0 | 13 | 2 | US-10-192-424-1 | Sequence 1, Appli |
| 33 | 34 | 100.0 | 13 | 2 | US-10-171-343-1 | Sequence 1, Appli |
| 34 | 34 | 100.0 | 13 | 2 | US-10-337-075-1 | Sequence 1, Appli |
| 35 | 34 | 100.0 | 20 | 2 | US-09-747-287A-198 | Sequence 198, App |
| 36 | 34 | 100.0 | 20 | 2 | US-09-394-019C-150 | Sequence 150, App |
| 37 | 34 | 100.0 | 21 | 2 | US-09-394-019C-395 | Sequence 395, App |
| 38 | 34 | 100.0 | 21 | 1 | US-08-659-984A-18 | Sequence 18, Appl |
| 39 | 34 | 100.0 | 21 | 2 | US-08-802-981-112 | Sequence 112, App |
| 40 | 34 | 100.0 | 21 | 2 | US-08-660-531-18 | Sequence 18, Appl |
| 41 | 34 | 100.0 | 21 | 2 | US-09-404-578-18 | Sequence 18, Appl |
| 42 | 34 | 100.0 | 21 | 2 | US-09-747-287A-172 | Sequence 172, App |
| 43 | 34 | 100.0 | 21 | 2 | US-09-747-287A-173 | Sequence 173, App |
| 44 | 34 | 100.0 | 21 | 2 | US-09-394-019C-125 | Sequence 125, App |
| 45 | 34 | 100.0 | 21 | 2 | US-09-394-019C-370 | Sequence 370, App |

ALIGNMENTS

RESULT 1
US-09-668-314C-71
Sequence 71, Application US/09668314C
; Patent No. 6844148
; GENERAL INFORMATION:
; APPLICANT: Gurney, et al
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 28341/6280NCP
; CURRENT APPLICATION NUMBER: US/09/668,314C
; CURRENT FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/169,232
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 71
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-668-314C-71

Query Match             100.0%;  Score 34;  DB 2;  Length 8;
Best Local Similarity   100.0%;  Pred. No. 4.6e+05;
Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVNLDAE 7
              |||||||
Db          1 EVNLDAE 7

RESULT 2
US-08-802-981-219
Sequence 219, Application US/08802981
; Patent No. 6037137
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of Enzyme

; PRIOR APPLICATION NUMBER: 60/292,591
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 60/316,115
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 257
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Beta-Secretase Cleavage Site
US-10-480-954-257

Query Match                100.0%; Score 34; DB 5; Length 8;
Best Local Similarity      100.0%; Pred. No. 1.7e+06;
Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy         1 EVNLDAE 7.
             |||||||
Db         1 EVNLDAE 7

RESULT 3
US-10-817-979-71
; Sequence 71, Application US/10817979
; Publication No. US2005019639 8A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, et al
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/40065
; CURRENT APPLICATION NUMBER: US/10/817,979
; CURRENT FILING DATE: 2004-04-05
; PRIOR APPLICATION NUMBER: US 09/668,314
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/169,232
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 71
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-817-979-71

Query Match                100.0%; Score 34; DB 5; Length 8;
Best Local Similarity      100.0%; Pred. No. 1.7e+06;
Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy         1 EVNLDAE 7
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Db         1 EVNLDAE 7

RESULT 4
US-09-896-874-8
; Sequence 8, Application US/09896874
; Patent No. US2002016320A1
; GENERAL INFORMATION:
; APPLICANT: Fang, Lawrence Y.

; APPLICANT: John, Varghese
; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
; FILE REFERENCE: 13615.40USU1
; CURRENT APPLICATION NUMBER: US/09/896,874
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,323
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-896-874-8

Query Match                100.0%; Score 34; DB 3; Length 9;
Best Local Similarity      100.0%; Pred. No. 1.7e+06;
Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy         1 EVNLDAE 7
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Db         2 EVNLDAE 8

RESULT 5
US-09-816-876-4
; Sequence 4, Application US/09816876
; Publication No. US2002019403A1
; GENERAL INFORMATION:
; APPLICANT: Hom, Roy
; APPLICANT: Mamo, Shumeye
; APPLICANT: Tung, Jay
; APPLICANT: Gailunas, Andrea
; APPLICANT: Varghese, John
; APPLICANT: Fang, Larry
; TITLE OF INVENTION: Methods to Treat Alzheimer's Disease
; FILE REFERENCE: 01-1736-D
; CURRENT APPLICATION NUMBER: US/09/816,876
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/191,528
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-816-876-4

Query Match                100.0%; Score 34; DB 3; Length 9;
Best Local Similarity      100.0%; Pred. No. 1.7e+06;
Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy         1 EVNLDAE 7
             |||||||
Db         2 EVNLDAE 8

RESULT 6
US-09-896-139-8
; Sequence 8, Application US/09896139
; Patent No. US2002012 8255A1
; GENERAL INFORMATION:
; APPLICANT: Beck, James P.
; APPLICANT: Fang, Lawrence Y.
; APPLICANT: Freskos, John N.
; APPLICANT: Gailunas, Andrea
; APPLICANT: Hom, Roy
; APPLICANT: Jagodzinska, Barbara

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OM protein - protein search, using sw model

Run on: March 15, 2006, 20:18:47 ; Search time 120 Seconds
(without alignments)
24.373 Million cell updates/sec

Title:          US-10-721-297-10
Perfect score:  34
Sequence:       1 EVNLDAE 7
Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters:        1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : Published Applications AA_Main:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
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| 1 | 34 | 100.0 | 7 | 5 | US-10-726-967A-59 | Sequence 59, Appli |
| 2 | 34 | 100.0 | 8 | 5 | US-10-480-954-257 | Sequence 257, App |
| 3 | 34 | 100.0 | 8 | 5 | US-10-817-979-71 | Sequence 71, Appl |
| 4 | 34 | 100.0 | 8 | 5 | US-09-896-874-8 | Sequence 8, Appli |
| 5 | 34 | 100.0 | 9 | 5 | US-09-816-876-4 | Sequence 4, Appli |
| 6 | 34 | 100.0 | 9 | 5 | US-09-896-139-8 | Sequence 8, Appli |
| 7 | 34 | 100.0 | 9 | 5 | US-09-895-843-8 | Sequence 8, Appli |
| 8 | 34 | 100.0 | 9 | 3 | US-09-908-943A-113 | Sequence 113, App |
| 9 | 34 | 100.0 | 9 | 3 | US-09-895-871-8 | Sequence 8, Appli |
| 10 | 34 | 100.0 | 9 | 3 | US-09-874-350A-209 | Sequence 209, App |
| 11 | 34 | 100.0 | 9 | 3 | US-10-192-625-8 | Sequence 8, Appli |
| 12 | 34 | 100.0 | 9 | 3 | US-10-192-424-8 | Sequence 8, Appli |
| 13 | 34 | 100.0 | 9 | 4 | US-10-183-126A-8 | Sequence 8, Appli |
| 14 | 34 | 100.0 | 9 | 4 | US-10-171-343-8 | Sequence 8, Appli |
| 15 | 34 | 100.0 | 9 | 4 | US-10-264-707-8 | Sequence 8, Appli |
| 16 | 34 | 100.0 | 9 | 4 | US-10-066-319-4 | Sequence 4, Appli |
| 17 | 34 | 100.0 | 9 | 4 | US-10-337-075-8 | Sequence 8, Appli |
| 18 | 34 | 100.0 | 9 | 4 | US-10-160-777-8 | Sequence 8, Appli |
| 19 | 34 | 100.0 | 9 | 4 | US-10-192-543-8 | Sequence 8, Appli |
| 20 | 34 | 100.0 | 9 | 4 | US-10-299-739-8 | Sequence 8, Appli |
| 21 | 34 | 100.0 | 9 | 4 | US-10-685-898-107 | Sequence 107, App |
| 22 | 34 | 100.0 | 9 | 4 | US-10-658-959A-8 | Sequence 8, Appli |
| 23 | 34 | 100.0 | 9 | 5 | US-10-801-487-113 | Sequence 113, App |
| 24 | 34 | 100.0 | 9 | 5 | US-10-801-938-113 | Sequence 113, App |
| 25 | 34 | 100.0 | 9 | 5 | US-10-801-509-113 | Sequence 113, App |
| 26 | 34 | 100.0 | 9 | 5 | US-10-801-486-113 | Sequence 113, App |
| 27 | 34 | 100.0 | 9 | 5 | US-10-621-311-1 | Sequence 1, Appli |
| 28 | 34 | 100.0 | 9 | 5 | US-10-828-582-8 | Sequence 8, Appli |
| 29 | 34 | 100.0 | 9 | 5 | US-10-801-493-113 | Sequence 113, App |
| 30 | 34 | 100.0 | 9 | 5 | US-11-075-161-8 | Sequence 8, Appli |
| 31 | 34 | 100.0 | 9 | 6 | US-11-090-866-52 | Sequence 52, Appl |
| 32 | 34 | 100.0 | 9 | 6 | US-11-090-866-83 | Sequence 83, Appl |
| 33 | 34 | 100.0 | 9 | 6 | US-11-089-918-52 | Sequence 52, Appl |
| 34 | 34 | 100.0 | 9 | 6 | US-11-089-918-83 | Sequence 83, Appl |
| 35 | 34 | 100.0 | 9 | 6 | US-11-076-161-8 | Sequence 8, Appli |
| 36 | 34 | 100.0 | 9 | 6 | US-11-069-377-52 | Sequence 52, Appl |
| 37 | 34 | 100.0 | 9 | 6 | US-11-069-377-83 | Sequence 83, Appl |
| 38 | 34 | 100.0 | 9 | 6 | US-11-090-872-52 | Sequence 52, Appl |
| 39 | 34 | 100.0 | 9 | 6 | US-11-090-872-83 | Sequence 83, Appl |
| 40 | 34 | 100.0 | 9 | 6 | US-11-090-399-52 | Sequence 52, Appl |
| 41 | 34 | 100.0 | 9 | 6 | US-11-090-399-83 | Sequence 83, Appl |
| 42 | 34 | 100.0 | 9 | 6 | US-11-042-695-8 | Sequence 8, Appli |
| 43 | 34 | 100.0 | 9 | 6 | US-11-075-294-10 | Sequence 10, Appl |
| 44 | 34 | 100.0 | 9 | 6 | US-11-074-828-10 | Sequence 10, Appl |
| 45 | 34 | 100.0 | 9 | 6 | US-11-075-312-10 | Sequence 10, Appl |

ALIGNMENTS

RESULT 1
US-10-726-967A-59
; Sequence 59, Application US/10726967A
; Publication No. US2005007445A1
; GENERAL INFORMATION:
; APPLICANT: Ballinger, Marcus
; TITLE OF INVENTION: Constructs for Homogenously Processed Preparations of Beta Site
; FILE REFERENCE: 200435-0021
; CURRENT APPLICATION NUMBER: US/10/726,967A
; CURRENT FILING DATE: 2003-12-02
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 59
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Engineered BACE1 autoproteolysis site
US-10-726-967A-59

Query Match             100.0%;  Score 34;  DB 5;  Length 7;
Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVNLDAE 7
              |||||||
Db          1 EVNLDAE 7

RESULT 2
US-10-480-954-257
; Sequence 257, Application US/10480954
; Publication No. US2005003219OA1
; GENERAL INFORMATION:
; APPLICANT: Brady, Stephen F.
; APPLICANT: Bruce, James E.
; APPLICANT: Chen-Dodson, Elizabeth
; APPLICANT: Garsky, Victor
; APPLICANT: Li, Yueming
; APPLICANT: Sardana, Mohinder
; APPLICANT: Shafer, Jules A.
; APPLICANT: Tang, Xiaoting
; TITLE OF INVENTION: BETA-SECRETASE SUBSTRATES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 20886YP
; CURRENT APPLICATION NUMBER: US/10/480,954
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: PCT/US02/15590
; PRIOR FILING DATE: 2002-05-17

APPLICANT: NEITZ, R. JEFFREY
; TITLE OF INVENTION: SUBSTITUTED UREA AND CARBAMATE, PHENACYL-2-HYDROXY-3-DIAMINOALKANE ASPARTYL-PROTEASE INHIBI
; AND BENZAMIDE-2-HYDROXY-3-DIAMINOALKANE
; FILE REFERENCE: 09511.0005-00000
; CURRENT APPLICATION NUMBER: US/11/075,292
; CURRENT FILING DATE: 2005-03-09
; PRIOR APPLICATION NUMBER: 60/622,589
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: 60/591,857
; PRIOR FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: 60/575,829
; PRIOR FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: 60/551,192
; PRIOR FILING DATE: 2004-03-09
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 3.3
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-11-075-292-10

Query Match　　100.0%;　Score 34;　DB 7;　Length 9;
Best Local Similarity　100.0%;　Pred. No. 1.3e+05;
Matches　7;　Conservative　0;　Mismatches　0;　Indels　0;　Gaps　0;

Qy　　1　EVNLDAE　7
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Db　　2　EVNLDAE　8

RESULT 3
US-11-090-520-8
; Sequence 8, Application US20050267199A1
; Publication No. US20050267199A1
; GENERAL INFORMATION:
; APPLICANT: Hom, Roy
; APPLICANT: Tucker, John
; APPLICANT: John, Varghese
; APPLICANT: Shah, Neerav
; TITLE OF INVENTION: 2-Amino- and 2-Thio- Substituted 1,3-Diaminopropanes
; FILE REFERENCE: 04-244-A
; CURRENT APPLICATION NUMBER: US/11/090,520
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/556,461
; PRIOR FILING DATE: 2004-03-25
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-11-090-520-8

Query Match　　100.0%;　Score 34;　DB 7;　Length 9;
Best Local Similarity　100.0%;　Pred. No. 1.3e+05;
Matches　7;　Conservative　0;　Mismatches　0;　Indels　0;　Gaps　0;

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Db　　2　EVNLDAE　8

RESULT 4
US-11-038-790-10
; Sequence 10, Application US/11038790
; Publication No. US20060014790A1
; GENERAL INFORMATION:

APPLICANT: JOHN, VARGHESE
; APPLICANT: HOM, ROY
; APPLICANT: SEALY, JENNIFER
; APPLICANT: AQUINO, JOSE
; APPLICANT: PROBST, GARY
; APPLICANT: TUNG, JAY
; APPLICANT: FANG, LAWRENCE
; TITLE OF INVENTION: METHODS OF TREATMENT OF AMYLOIDOSIS USING
; TITLE OF INVENTION: SPIROCYCLOHEXANE ASPARTYL-PROTEASE INHIBITORS
; FILE REFERENCE: 09511.0004-00000
; CURRENT APPLICATION NUMBER: US/11/038,790
; CURRENT FILING DATE: 2005-01-21
; PRIOR APPLICATION NUMBER: 60/619,948
; PRIOR FILING DATE: 2004-10-20
; PRIOR APPLICATION NUMBER: 60/619,947
; PRIOR FILING DATE: 2004-10-20
; PRIOR APPLICATION NUMBER: 60/619,917
; PRIOR FILING DATE: 2004-10-20
; PRIOR APPLICATION NUMBER: 60/591,885
; PRIOR FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: 60/591,908
; PRIOR FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: 60/591,858
; PRIOR FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: 60/575,799
; PRIOR FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: 60/575,858
; PRIOR FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: 60/575,798
; PRIOR FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: 60/537,551
; PRIOR FILING DATE: 2004-01-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 3.3
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-11-038-790-10

Query Match　　100.0%;　Score 34;　DB 7;　Length 9;
Best Local Similarity　100.0%;　Pred. No. 1.3e+05;
Matches　7;　Conservative　0;　Mismatches　0;　Indels　0;　Gaps　0;

Qy　　1　EVNLDAE　7
　　　　　|||||||
Db　　2　EVNLDAE　8

RESULT 5
US-11-075-445-10
; Sequence 10, Application US/11075445
; Publication No. US20060014737A1
; GENERAL INFORMATION:
; APPLICANT: JOHN, VARGHESE
; APPLICANT: HOM, ROY
; APPLICANT: SEALEY, JENNIFER
; APPLICANT: TUCKER, JOHN
; TITLE OF INVENTION: METHODS OF TREATMENT OF AMYLOIDOSIS USING BI-ARYL ASPARTYL PROTEA
; TITLE OF INVENTION: INHIBITORS
; FILE REFERENCE: 09511.0006-00000
; CURRENT APPLICATION NUMBER: US/11/075,445
; CURRENT FILING DATE: 2005-03-09
; PRIOR APPLICATION NUMBER: 60/551,205
; PRIOR FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: 60/551,013
; PRIOR FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: 60/575,964
; PRIOR FILING DATE: 2004-06-02

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on:               March 15, 2006, 20:19:57 ; Search time 15 Seconds
                      (without alignments)
                      13.357 Million cell updates/sec

Title:                US-10-721-297-10
Perfect score:        34
Sequence:             1 EVNLDAE 7
Scoring table:        BLOSUM62
                      Gapop 10.0 , Gapext 0.5

Searched:             169630 seqs, 28622889 residues
Total number of hits satisfying chosen parameters:        169630

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Published Applications AA New:*
                 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
                 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
                 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
                 4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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                 7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
                 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Match Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 34 | 100.0 | 7 | 6 | US-10-895-861-21 | Sequence 21, Appli |
| 2 | 34 | 100.0 | 7 | 6 | US-11-075-292-10 | Sequence 10, Appli |
| 3 | 34 | 100.0 | 9 | 7 | US-11-090-520-8 | Sequence 8, Appli |
| 4 | 34 | 100.0 | 9 | 7 | US-11-038-790-10 | Sequence 10, Appli |
| 5 | 34 | 100.0 | 9 | 7 | US-11-075-445-10 | Sequence 10, Appli |
| 6 | 34 | 100.0 | 9 | 7 | US-11-218-879-8 | Sequence 8, Appli |
| 7 | 34 | 100.0 | 10 | 7 | US-10-895-861-2 | Sequence 2, Appli |
| 8 | 34 | 100.0 | 11 | 6 | US-10-348-595-2 | Sequence 2, Appli |
| 9 | 34 | 100.0 | 11 | 6 | US-10-348-595-4 | Sequence 4, Appli |
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| 11 | 34 | 100.0 | 13 | 7 | US-11-090-520-1 | Sequence 1, Appli |
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| 14 | 34 | 100.0 | 13 | 7 | US-11-218-879-1 | Sequence 1, Appli |
| 15 | 34 | 100.0 | 6 | 6 | US-10-348-595-7 | Sequence 7, Appli |
| 16 | 34 | 100.0 | 23 | 6 | US-11-075-292-11 | Sequence 11, Appli |
| 17 | 34 | 100.0 | 7 | 7 | US-11-090-520-9 | Sequence 9, Appli |
| 18 | 34 | 100.0 | 7 | 7 | US-11-038-790-11 | Sequence 11, Appli |
| 19 | 34 | 100.0 | 7 | 7 | US-11-075-445-11 | Sequence 11, Appli |
| 20 | 34 | 100.0 | 7 | 7 | US-11-218-879-9 | Sequence 9, Appli |
| 21 | 34 | 100.0 | 7 | 7 | US-11-075-292-8 | Sequence 8, Appli |
| 22 | 34 | 100.0 | 7 | 7 | US-11-090-520-6 | Sequence 6, Appli |
| 23 | 34 | 100.0 | 7 | 7 | US-11-038-790-8 | Sequence 8, Appli |
| 24 | 34 | 100.0 | 7 | 7 | US-11-075-445-8 | Sequence 8, Appli |
| 25 | 34 | 100.0 | 33 | 7 | US-11-218-879-6 | Sequence 6, Appli |
| 26 | 34 | 100.0 | 34 | 7 | US-11-075-292-6 | Sequence 6, Appli |
| 27 | 34 | 100.0 | 34 | 7 | US-11-090-520-4 | Sequence 4, Appli |
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| 31 | 28 | 82.4 | 147 | 7 | US-11-096-568A-15094 | Sequence 15094, A |
| 32 | 28 | 82.4 | 181 | 7 | US-11-096-568A-15093 | Sequence 15093, A |
| 33 | 28 | 82.4 | 206 | 7 | US-11-096-568A-15092 | Sequence 15092, A |
| 34 | 27 | 79.4 | 226 | 7 | US-11-096-568A-4752 | Sequence 4752, Ap |
| 35 | 27 | 79.4 | 231 | 7 | US-11-096-568A-15700 | Sequence 15700, A |
| 36 | 27 | 79.4 | 250 | 7 | US-11-096-568A-32295 | Sequence 32295, A |
| 37 | 27 | 79.4 | 251 | 7 | US-11-096-568A-4751 | Sequence 4751, Ap |
| 38 | 27 | 79.4 | 254 | 7 | US-11-096-568A-15699 | Sequence 15699, A |
| 39 | 27 | 79.4 | 260 | 7 | US-11-096-568A-29072 | Sequence 29072, A |
| 40 | 27 | 79.4 | 289 | 7 | US-11-096-568A-11346 | Sequence 11346, A |
| 41 | 27 | 79.4 | 322 | 7 | US-11-096-568A-11345 | Sequence 11345, A |
| 42 | 27 | 79.4 | 328 | 7 | US-11-096-568A-11344 | Sequence 11344, A |
| 43 | 26 | 76.5 | 11 | 6 | US-10-348-595-1 | Sequence 1, Appli |
| 44 | 26 | 76.5 | 11 | 6 | US-10-348-595-3 | Sequence 3, Appli |
| 45 | 26 | 76.5 | 13 | 7 | US-11-075-292-4 | Sequence 4, Appli |

ALIGNMENTS

RESULT 1
US-10-895-861-21
; Sequence 21, Application US/10895861
; Publication No. US20060019368A1
; GENERAL INFORMATION:
;  APPLICANT: BALLINGER, Marcus
;  APPLICANT: RANDAL, Michael L.
;  TITLE OF INVENTION: CONSTRUCTS FOR HOMOGENOUSLY PROCESSED
;  TITLE OF INVENTION: PREPARATIONS OF BETA SITE APP-CLEAVING ENZYME
;  FILE REFERENCE: 39750-0027US
;  CURRENT APPLICATION NUMBER: US/10/895,861
;  CURRENT FILING DATE: 2004-07-20
;  PRIOR APPLICATION NUMBER: US 60/430,984
;  PRIOR FILING DATE: 2002-12-04
;  PRIOR APPLICATION NUMBER: US 10/726,967
;  PRIOR FILING DATE: 2003-12-02
;  PRIOR APPLICATION NUMBER: PCT to be assigned
;  PRIOR FILING DATE: 2004-07-07
;  NUMBER OF SEQ ID NOS: 98
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 21
;  LENGTH: 7
;  TYPE: PRT
;  ORGANISM: homo sapiens
US-10-895-861-21

    Query Match             100.0%;  Score 34;  DB 6;  Length 7;
    Best Local Similarity   100.0%;  
    Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVNLDAE 7
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Db          1 EVNLDAE 7

RESULT 2
US-11-075-292-10
; Sequence 10, Application US/11075292
; Publication No. US20050261273A1
; GENERAL INFORMATION:
;  APPLICANT: JOHN, VARGHESE
;  APPLICANT: MAILLARD, MICHEL
;  APPLICANT: TUCKER, JOHN
;  APPLICANT: AQUINO, JOSE
;  APPLICANT: HOM, ROY
;  APPLICANT: TUNG, JAY
;  APPLICANT: DRESSEN, DARREN
;  APPLICANT: SHAH, NEERAV